

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5
- (i) APPLICANT:
- (B) NAME: CREATIVE BIOMOLCULES, INC
- (C) STREET: 45 SOUTH STREET
- (D) STATE: HOPKINTON
- 10 (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 01748
- (G) TELEPHONE: (508)-435-9001
- (H) TELEFAX: (508)-435-0992
- (I) TELEX:
- 15
- (i) APPLICANT:
- (B) NAME: LUDWIG INSTITUTE FOR CANCER RESEARCH
- (C) STREET: 1345 AVENUE OF THE AMERICAS
- 20 (D) STATE: NY
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 10105
- (G) TELEPHONE: (212)-765-3000
- (H) TELEFAX:
- (I) TELEX:
- 25
- (ii) TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL  
SURFACE RECEPTORS AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 15
- 30
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
THIBEAULT
- 35 (B) STREET: 53 STATE STREET
- (C) CITY: BOSTON
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02109
- 40
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 45
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- 50
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: PITCHER, EDMUND R.
- (B) REGISTRATION NUMBER: 27,829
- (C) REFERENCE/DOCKET NUMBER: CRP-097PC
- 55
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (617) 248-7000
- (B) TELEFAX: (617) 248-7100
- 60

FOR "E4528660"

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1509
- (D) OTHER INFORMATION: /product= "Human ALK1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	ATG ACC TTG GGC TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC	48
	Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
	1 5 10 15	
25	TTG GTG ACC CAG GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG	96
	Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
	20 25 30	
30	ACC TGC ACG TGT GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG	144
	Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
	35 40 45	
35	GCC TGG TGC ACA GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG	192
	Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
	50 55 60	
40	GAA CAT CGG GGC TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC	240
	Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
	65 70 75 80	
45	CCC ACC GAG TTC GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC	288
	Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
	85 90 95	
50	CAC AAC GTG TCC CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG	336
	His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
	100 105 110	
55	CCG GGA ACA GAT GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC	384
	Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
	115 120 125	
60	TTG CTG GCC CTG GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA	432
	Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
	130 135 140	
65	CGG AGG CAG GAG AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC	480
	Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser	
	145 150 155 160	
70	AGT CTC ATC CTG AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC	528

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	Ser	Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	
					165					170					175		
5	CTC	CTG	GAC	AGT	GAC	TGC	ACC	ACA	GGG	AGT	GGC	TCA	GGG	CTC	CCC	TTC	576
	Leu	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	
				180					185					190			
10	CTG	GTG	CAG	AGG	ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	624
	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	
			195					200					205				
15	GGA	AAA	GGC	CGC	TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG	TGG	CAC	GGT	GAG	672
	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	
		210					215					220					
20	AGT	GTG	GCC	GTC	AAG	ATC	TTC	TCC	TCG	AGG	GAT	GAA	CAG	TCC	TGG	TTC	720
	Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	
	225					230					235					240	
25	CGG	GAG	ACT	GAG	ATC	TAT	AAC	ACA	GTA	TTG	CTC	AGA	CAC	GAC	AAC	ATC	768
	Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	
					245					250					255		
30	CTA	GGC	TTC	ATC	GCC	TCA	GAC	ATG	ACC	TCC	CGC	AAC	TCG	AGC	ACG	CAG	816
	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	
				260				265						270			
35	CTG	TGG	CTC	ATC	ACG	CAC	TAC	CAC	GAG	CAC	GGC	TCC	CTC	TAC	GAC	TTT	864
	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	
			275				280						285				
40	CTG	CAG	AGA	CAG	ACG	CTG	GAG	CCC	CAT	CTG	GCT	CTG	AGG	CTA	GCT	GTG	912
	Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	
		290					295					300					
45	TCC	GCG	GCA	TGC	GGC	CTG	GCG	CAC	CTG	CAC	GTG	GAG	ATC	TTC	GGT	ACA	960
	Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	
	305					310					315					320	
50	CAG	GGC	AAA	CCA	GCC	ATT	GCC	CAC	CGC	GAC	TTC	AAG	AGC	CGC	AAT	GTG	1008
	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	
					325				330						335		
55	CTG	GTC	AAG	AGC	AAC	CTG	CAG	TGT	TGC	ATC	GCC	GAC	CTG	GGC	CTG	GCT	1056
	Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
				340				345						350			
60	GTG	ATG	CAC	TCA	CAG	GGC	AGC	GAT	TAC	CTG	GAC	ATC	GGC	AAC	AAC	CCG	1104
	Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	
			355					360					365				
65	AGA	GTG	GGC	ACC	AAG	CGG	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAC	GAG	CAG	1152
	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln	
		370					375					380					
70	ATC	CGC	ACG	GAC	TGC	TTT	GAG	TCC	TAC	AAG	TGG	ACT	GAC	ATC	TGG	GCC	1200
	Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	
					385		390				395					400	
75	TTT	GGC	CTG	GTG	CTG	TGG	GAG	ATT	GCC	CGC	CGG	ACC	ATC	GTG	AAT	GGC	1248

"CTG" 4523560

Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly  
405 410 415

5 ATC GTG GAG GAC TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC 1296  
Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp  
420 425 430

10 CCC AGC TTT GAG GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC 1344  
Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr  
435 440 445

15 CCC ACC ATC CCT AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA 1392  
Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu  
450 455 460

GCT CAG ATG ATG CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC 1440  
Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu  
465 470 475 480

20 ACC GCG CTG CGG ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA 1488  
Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro  
485 490 495

25 GAG AAG CCT AAA GTG ATT CAA 1509  
Glu Lys Pro Lys Val Ile Gln  
500

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 503 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala  
1 5 10 15

Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val  
20 25 30

45 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly  
35 40 45

50 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln  
50 55 60

Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg  
65 70 75 80

55 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn  
85 90 95

His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln  
100 105 110

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TOPOT E452860

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	CCG	TCC	CCT	GGC	CAA	GCT	GTG	GAG	TGC	TGC	CAA	GGG	GAC	TGG	TGT	AAC	403
	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	Asp	Trp	Cys	Asn	
	85					90					95					100	
5	AGG	AAC	ATC	ACG	GCC	CAG	CTG	CCC	ACT	AAA	GGA	AAA	TCC	TTC	CCT	GGA	451
	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys	Ser	Phe	Pro	Gly	
					105					110					115		
10	ACA	CAG	AAT	TTC	CAC	TTG	GAG	GTT	GGC	CTC	ATT	ATT	CTC	TCT	GTA	GTG	499
	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	Leu		Val	Val	
				120					125					130			
15	TTC	GCA	GTA	TGT	CTT	TTA	GCC	TGC	CTG	CTG	GGA	GTT	GCT	CTC	CGA	AAA	547
	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val	Ala	Leu	Arg	Lys	
			135					140					145				
20	TTT	AAA	AGG	CGC	AAC	CAA	GAA	CGC	CTC	AAT	CCC	CGA	GAC	GTG	GAG	TAT	595
	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg	Asp	Val	Glu	Tyr	
		150					155					160					
25	GGC	ACT	ATC	GAA	GGG	CTC	ATC	ACC	ACC	AAT	GTT	GGA	GAC	AGC	ACT	TTA	643
	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	Asp	Ser	Thr	Leu	
	165					170					175					180	
30	GCA	GAT	TTA	TTG	GAT	CAT	TCG	TGT	ACA	TCA	GGA	AGT	GGC	TCT	GGT	CTT	691
	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	Gly	Ser	Gly	Leu	
					185					190					195		
35	CCT	TTT	CTG	GTA	CAA	AGA	ACA	GTG	GCT	CGC	CAG	ATT	ACA	CTG	TTG	GAG	739
	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	Thr	Leu	Leu	Glu	
				200					205					210			
40	TGT	GTC	GGG	AAA	GGC	AGG	TAT	GGT	GAG	GTG	TGG	AGG	GGC	AGC	TGG	CAA	787
	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	Gln	
			215					220					225				
45	GGG	GAA	AAT	GTT	GCC	GTG	AAG	ATC	TTC	TCC	TCC	CGT	GAT	GAG	AAG	TCA	835
	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Lys	Ser	
		230					235					240					
50	TGG	TTC	AGG	GAA	ACG	GAA	TTG	TAC	AAC	ACT	GTG	ATG	CTG	AGG	CAT	GAA	883
	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	Leu	Arg	His	Glu	
	245					250					255					260	
55	AAT	ATC	TTA	GGT	TTC	ATT	GCT	TCA	GAC	ATG	ACA	TCA	AGA	CAC	TCC	AGT	931
	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	His	Ser	Ser	
					265					270					275		
60	ACC	CAG	CTG	TGG	TTA	ATT	ACA	CAT	TAT	CAT	GAA	ATG	GGA	TCG	TTG	TAC	979
	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	Gly	Ser	Leu	Tyr	
				280					285					290			
65	GAC	TAT	CTT	CAG	CTT	ACT	ACT	CTG	GAT	ACA	GTT	AGC	TGC	CTT	CGA	ATA	1027
	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser	Cys	Leu	Arg	Ile	
			295					300					305				
70	GTG	CTG	TCC	ATA	GCT	AGT	GGT	CTT	GCA	CAT	TTG	CAC	ATA	GAG	ATA	TTT	1075
	Val	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Ile	Glu	Ile	Phe	
		310					315					320					

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	GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA	1123
	Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys	
	325 330 335 340	
5	AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC	1171
	Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly	
	345 350 355	
10	CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC	1219
	Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn	
	360 365 370	
15	AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT	1267
	Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp	
	375 380 385	
20	GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT	1315
	Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile	
	390 395 400	
25	TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC	1363
	Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser	
	405 410 415 420	
30	AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC	1411
	Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro	
	425 430 435	
35	AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA	1459
	Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln	
	440 445 450	
40	CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC	1507
	Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr	
	455 460 465	
45	TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA	1555
	Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala	
	470 475 480	
50	AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT	1603
	Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn	
	485 490 495 500	
55	TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA	1650
	Ser Leu Asp Lys Leu Lys Thr Asp Cys	
	505 510	
60	GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT	1710
	TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC	1770
	GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA	1830
	ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA	1890
	AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG	1950
	GCTTTGCATA GCTTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT	2010

09545660



GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTCTTT ATTGCACTAG GAATTCTTTG 2070  
 5 CATTCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT 2130  
 GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA 2190  
 TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTA CAATGATGCC GAACATTAGG 2250  
 10 AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTTACAA 2310  
 AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA 2370  
 ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT 2430  
 15 TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACCT TTTTTCAGTT CATATGCAGA 2490  
 ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA 2550  
 20 TTTTCAGTAG ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC 2610  
 ATTACGTGCA TTAAACTCT GCCAGAAAAA AATACTATT TTGTTTAAAT CTACTTTTTG 2670  
 TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTT AAGTCAAAAA AAAA 2724  
 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 509 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu  
 1 5 10 15  
 40 Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu  
 20 25 30  
 45 Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys  
 35 40 45  
 Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His  
 50 55 60  
 50 Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr  
 65 70 75 80  
 Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly  
 85 90 95  
 55 Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys  
 100 105 110  
 60 Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile  
 115 120 125

09984310100

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val  
130 135 140

5 Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg  
145 150 155 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly  
165 170 175

10 Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser  
180 185 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile  
195 200 205

15 Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg  
210 215 220

20 Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg  
225 230 235 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met  
245 250 255

25 Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser  
260 265 270

Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met  
275 280 285

Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser  
290 295 300

35 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His  
305 310 315 320

Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp  
325 330 335

40 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile  
340 345 350

Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu  
355 360 365

45 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro  
370 375 380

50 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys  
385 390 395 400

Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg  
405 410 415

55 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr  
420 425 430

60 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val  
435 440 445

093354 101301

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp  
 450 455 460

5 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln  
 465 470 475 480

Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr  
 485 490 495

10 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys  
 500 505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 310..1908
- (D) OTHER INFORMATION: /product= "Human ALK3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT 60

35 CAGTTTAATA CTGTCTTGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA 120

AATCAGAAGT ACAGTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180

40 TTGAAGTCAT TGCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240

TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300

AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348

45 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala  
 1 5 10

TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396

50 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met  
 15 20 25

CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444

Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu  
 30 35 40 45

55 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492

Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys  
 50 55 60

60 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC AGA TGC ATA 540

	Tyr	Cys	Ser	Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	
				65					70					75			
5	ACT	AAT	GGA	CAT	TGC	TTT	GCC	ATC	ATA	GAA	GAA	GAT	GAC	CAG	GGA	GAA	588
	Thr	Asn	Gly	His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	
			80					85					90				
10	ACC	ACA	TTA	GCT	TCA	GGG	TGT	ATG	AAA	TAT	GAA	GGA	TCT	GAT	TTT	CAG	636
	Thr	Thr	Leu	Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	
			95					100					105				
15	TGC	AAA	GAT	TCT	CCA	AAA	GCC	CAG	CTA	CGC	CGG	ACA	ATA	GAA	TGT	TGT	684
	Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	
	110					115					120					125	
20	CGG	ACC	AAT	TTA	TGT	AAC	CAG	TAT	TTG	CAA	CCC	ACA	CTG	CCC	CCT	GTT	732
	Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	
					130					135					140		
25	GTC	ATA	GGT	CCG	TTT	TTT	GAT	GGC	AGC	ATT	CGA	TGG	CTG	GTT	TTG	CTC	780
	Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	
				145				150					155				
30	ATT	TCT	ATG	GCT	GTC	TGC	ATA	ATT	GCT	ATG	ATC	ATC	TTC	TCC	AGC	TGC	828
	Ile	Ser	Met	Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	
			160					165					170				
35	TTT	TGT	TAC	AAA	CAT	TAT	TGC	AAG	AGC	ATC	TCA	AGC	AGA	CGT	CGT	TAC	876
	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	
			175				180					185					
40	AAT	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	TTT	ATT	CCA	GTT	GGA	GAA	TCA	924
	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	
	190					195					200					205	
45	CTA	AAA	GAC	CTT	ATT	GAC	CAG	TCA	CAA	AGT	TCT	GGT	AGT	GGG	TCT	GGA	972
	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	
					210					215					220		
50	CTA	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	GCC	AAA	CAG	ATT	CAG	ATG	GTC	1020
	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	
					225				230					235			
55	CGG	CAA	GTT	GGT	AAA	GGC	CGA	TAT	GGA	GAA	GTA	TGG	ATG	GGC	AAA	TGG	1068
	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	
			240					245					250				
60	CGT	GGC	GAA	AAA	GTG	GCG	GTG	AAA	GTA	TTC	TTT	ACC	ACT	GAA	GAA	GCC	1116
	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	
		255					260					265					
65	AGC	TGG	TTT	CGA	GAA	ACA	GAA	ATC	TAC	CAA	ACT	GTG	CTA	ATG	CGC	CAT	1164
	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	
						275					280					285	
70	GAA	AAC	ATA	CTT	GGT	TTC	ATA	GCG	GCA	GAC	ATT	AAA	GGT	ACA	GGT	TCC	1212
	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	
					290					295					300		
75	TGG	ACT	CAG	CTC	TAT	TTG	ATT	ACT	GAT	TAC	CAT	GAA	AAT	GGA	TCT	CTC	1260

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	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	
				305					310					315			
5	TAT	GAC	TTC	CTG	AAA	TGT	GCT	ACA	CTG	GAC	ACC	AGA	GCC	CTG	CTT	AAA	1308
	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	
			320					325					330				
10	TTG	GCT	TAT	TCA	GCT	GCC	TGT	GGT	CTG	TGC	CAC	CTG	CAC	ACA	GAA	ATT	1356
	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	
			335				340					345					
15	TAT	GGC	ACC	CAA	GGA	AAG	CCC	GCA	ATT	GCT	CAT	CGA	GAC	CTA	AAG	AGC	1404
	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	
						355					360					365	
20	AAA	AAC	ATC	CTC	ATC	AAG	AAA	AAT	GGG	AGT	TGC	TGC	ATT	GCT	GAC	CTG	1452
	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	
					370					375					380		
25	GGC	CTT	GCT	GTT	AAA	TTC	AAC	AGT	GAC	ACA	AAT	GAA	GTT	GAT	GTG	CCC	1500
	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	
				385					390					395			
30	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAA	CGC	TAC	ATG	GCT	CCC	GAA	GTG	CTG	1548
	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	
			400					405					410				
35	GAC	GAA	AGC	CTG	AAC	AAA	AAC	CAC	TTC	CAG	CCC	TAC	ATC	ATG	GCT	GAC	1596
	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	
			415				420					425					
40	ATC	TAC	AGC	TTC	GGC	CTA	ATC	ATT	TGG	GAG	ATG	GCT	CGT	CGT	TGT	ATC	1644
	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	
						435					440					445	
45	ACA	GGA	GGG	ATC	GTG	GAA	GAA	TAC	CAA	TTG	CCA	TAT	TAC	AAC	ATG	GTA	1692
	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	
					450					455					460		
50	CCG	AGT	GAT	CCG	TCA	TAC	GAA	GAT	ATG	CGT	GAG	GTT	GTG	TGT	GTC	AAA	1740
	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Val	Val	Cys	Val	Lys	
				465					470					475			
55	CGT	TTG	CGG	CCA	ATT	GTG	TCT	AAT	CGG	TGG	AAC	AGT	GAT	GAA	TGT	CTA	1788
	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	
			480					485					490				
60	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	TGC	TGG	GCC	CAC	AAT	CCA	GCC	1836
	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	
			495				500					505					
65	TCC	AGA	CTC	ACA	GCA	TTG	AGA	ATT	AAG	AAG	ACG	CTT	GCC	AAG	ATG	GTT	1884
	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	
						515					520				525		
70	GAA	TCC	CAA	GAT	GTA	AAA	ATC	TGATGGTTAA	ACCATCGGAG	GAGAACTCT							1935
	Glu	Ser	Gln	Asp	Val	Lys	Ile										
					530												
75	AGACTGCAAG	AACTGTTTTT	ACCCATGGCA	TGGGTGGAAT	TAGAGTGGAA	TAAGGATGTT											1995

AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTACACAG GCTGCTAATA TTAAACCTTT 2055  
 CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATCTT TATATATGGA 2115  
 5 CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA 2175  
 TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGTACTGAA TTGCCTGTTC 2235  
 10 ATAAAACGGT GCTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA 2295  
 AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA 2355  
 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC 2415  
 15 TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATCCTCTGC TGCCATTTGA 2475  
 ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG 2535  
 20 CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TACTTTGCA 2595  
 AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655  
 AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTCCTTC AACCACCATT TTTTTGTGG 2715  
 25 TTATTATTTT TGTACCGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC 2775  
 ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTGATA GCAATGTAAG 2835  
 30 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTAAAAGGG AAGTTATTTA 2895  
 TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC 2932

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

45 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe  
 1 5 10 15  
 50 Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly  
 20 25 30  
 Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val  
 35 40 45  
 55 Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser  
 50 55 60  
 Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly  
 65 70 75 80

60

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
405 410 415

5 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
420 425 430

Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
435 440 445

10 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
450 455 460

Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg  
465 470 475 480

15 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val  
485 490 495

20 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu  
500 505 510

Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln  
515 520 525

25 Asp Val Lys Ile  
530

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 187..1695
- (D) OTHER INFORMATION: /product= "Murine ALK6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGGCGGC AGAAGTTGCC GCGTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC 60

50 TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC 120

AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT 180

GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG 228  
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys  
1 5 10

AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA 276  
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu  
15 20 25 30



	CGT	TGT	AAA	TGC	CAC	CAC	CAC	TGT	CCG	GAA	GAC	TCA	GTC	AAC	AAT	ATC	324
	Arg	Cys	Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	
					35					40						45	
5	TGC	AGC	ACA	GAT	GGG	TAC	TGC	TTC	ACG	ATG	ATA	GAA	GAA	GAT	GAC	TCT	372
	Cys	Ser	Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	
				50					55					60			
10	GGA	ATG	CCT	GTT	GTC	ACC	TCT	GGA	TGT	CTA	GGA	CTA	GAA	GGG	TCA	GAT	420
	Gly	Met	Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	
			65					70					75				
15	TTT	CAA	TGT	CGT	GAC	ACT	CCC	ATT	CCT	CAT	CAA	AGA	AGA	TCA	ATT	GAA	468
	Phe	Gln	Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	
		80					85					90					
20	TGC	TGC	ACA	GAA	AGG	AAT	GAG	TGT	AAT	AAA	GAC	CTC	CAC	CCC	ACT	CTG	516
	Cys	Cys	Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	
	95				100						105					110	
25	CCT	CCT	CTC	AAG	GAC	AGA	GAT	TTT	GTT	GAT	GGG	CCC	ATA	CAC	CAC	AAG	564
	Pro	Pro	Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	
				115					120						125		
30	GCC	TTG	CTT	ATC	TCT	GTG	ACT	GTC	TGT	AGT	TTA	CTC	TTG	GTC	CTC	ATT	612
	Ala	Leu	Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	
				130				135					140				
35	ATT	TTA	TTC	TGT	TAC	TTC	AGG	TAT	AAA	AGA	CAA	GAA	GCC	CGA	CCT	CGG	660
	Ile	Leu	Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	
			145					150					155				
40	TAC	AGC	ATT	GGG	CTG	GAG	CAG	GAC	GAG	ACA	TAC	ATT	CCT	CCT	GGA	GAG	708
	Tyr	Ser	Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	
		160					165					170					
45	TCC	CTG	AGA	GAC	TTG	ATC	GAG	CAG	TCT	CAG	AGC	TCG	GGA	AGT	GGA	TCA	756
	Ser	Leu	Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	
	175				180						185					190	
50	GGC	CTC	CCT	CTG	CTG	GTC	CAA	AGG	ACA	ATA	GCT	AAG	CAA	ATT	CAG	ATG	804
	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	
				195					200						205		
55	GTG	AAG	CAG	ATT	GGA	AAA	GGC	CGC	TAT	GGC	GAG	GTG	TGG	ATG	GGA	AAG	852
	Val	Lys	Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	
				210				215					220				
60	TGG	CGT	GGA	GAA	AAG	GTG	GCT	GTG	AAA	GTG	TTC	TTC	ACC	ACG	GAG	GAA	900
	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	
			225					230					235				
65	GCC	AGC	TGG	TTC	CGA	GAG	ACT	GAG	ATA	TAT	CAG	ACG	GTC	CTG	ATG	CGG	948
	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	
		240					245					250					
70	CAT	GAG	AAT	ATT	CTG	GGG	TTC	ATT	GCT	GCA	GAT	ATC	AAA	GGG	ACT	GGG	996
	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	
	255				260						265					270	

	TCC	TGG	ACT	CAG	TTG	TAC	CTC	ATC	ACA	GAC	TAT	CAT	GAA	AAC	GGC	TCC	1044
	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	
					275					280					285		
5	CTT	TAT	GAC	TAT	CTG	AAA	TCC	ACC	ACC	TTA	GAC	GCA	AAG	TCC	ATG	CTG	1092
	Leu	Tyr	Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	
				290					295					300			
10	AAG	CTA	GCC	TAC	TCC	TCT	GTC	AGC	GGC	CTA	TGC	CAT	TTA	CAC	ACG	GAA	1140
	Lys	Leu	Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	
			305					310					315				
15	ATC	TTT	AGC	ACT	CAA	GGC	AAG	CCA	GCA	ATC	GCC	CAT	CGA	GAC	TTG	AAA	1188
	Ile	Phe	Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	
		320					325					330					
20	AGT	AAA	AAC	ATC	CTG	GTG	AAG	AAA	AAT	GGA	ACT	TGC	TGC	ATA	GCA	GAC	1236
	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	
	335					340					345					350	
25	CTG	GGC	TTG	GCT	GTC	AAG	TTC	ATT	AGT	GAC	ACA	AAT	GAG	GTT	GAC	ATC	1284
	Leu	Gly	Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	
					355					360					365		
30	CCA	CCC	AAC	ACC	CGG	GTT	GGC	ACC	AAG	CGC	TAT	ATG	CCT	CCA	GAA	GTG	1332
	Pro	Pro	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	
				370					375					380			
35	CTG	GAC	GAG	AGC	TTG	AAT	AGA	AAC	CAT	TTC	CAG	TCC	TAC	ATT	ATG	GCT	1380
	Leu	Asp	Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	
			385				390						395				
40	GAC	ATG	TAC	AGC	TTT	GGA	CTC	ATC	CTC	TGG	GAG	ATT	GCA	AGG	AGA	TGT	1428
	Asp	Met	Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	
		400					405					410					
45	GTT	TCT	GGA	GGT	ATA	GTG	GAA	GAA	TAC	CAG	CTT	CCC	TAT	CAC	GAC	CTG	1476
	Val	Ser	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	
	415					420					425					430	
50	GTG	CCC	AGT	GAC	CCT	TCT	TAT	GAG	GAC	ATG	AGA	GAA	ATT	GTG	TGC	ATG	1524
	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Ile	Val	Cys	Met	
					435					440					445		
55	AAG	AAG	TTA	CGG	CCT	TCA	TTC	CCC	AAT	CGA	TGG	AGC	AGT	GAT	GAG	TGT	1572
	Lys	Lys	Leu	Arg	Pro	Ser	Phe	Pro	Asn	Arg	Trp	Ser	Ser	Asp	Glu	Cys	
				450					455					460			
60	CTC	AGG	CAG	ATG	GGG	AAG	CTT	ATG	ACA	GAG	TGC	TGG	GCG	CAG	AAT	CCT	1620
	Leu	Arg	Gln	Met	Gly	Lys	Leu	Met	Thr	Glu	Cys	Trp	Ala	Gln	Asn	Pro	
			465				470						475				
65	GCC	TCC	AGG	CTG	ACG	GCC	CTG	AGA	GTT	AAG	AAA	ACC	CTT	GCC	AAA	ATG	1668
	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Val	Lys	Lys	Thr	Leu	Ala	Lys	Met	
		480					485					490					
70	TCA	GAG	TCC	CAG	GAC	ATT	AAA	CTC	TGACGTCAGA	TACTTGTGGA	CAGAGCAAGA						1722
	Ser	Glu	Ser	Gln	Asp	Ile	Lys	Leu									
	495					500											

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ATTCACAGA AGCATCGTTA GCGCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA 1782  
 GACTTTCCTG GAAGAGAGCA CCGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT 1842  
 CATGGCTTTC TGAGGAGGAG AACTGTTTG GGTAAGTTGT TCAAGATATG ATGCATGTTG 1902  
 CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTT ATAAAAAAAA 1952

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(2) INFORMATION FOR SEQ ID NO:8:

(i). SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu  
 1 5 10 15  
 Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys  
 20 25 30  
 Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser  
 35 40 45  
 Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met  
 50 55 60  
 Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln  
 65 70 75 80  
 Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys  
 85 90 95  
 Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
 100 105 110  
 Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu  
 115 120 125  
 Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu  
 130 135 140  
 Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser  
 145 150 155 160  
 Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu  
 165 170 175  
 Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
 180 185 190  
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
 195 200 205

60

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Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
 210 215 220  
 5 Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser  
 225 230 235 240  
 Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu  
 245 250 255  
 10 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
 260 265 270  
 Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
 275 280 285  
 15 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu  
 290 295 300  
 20 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe  
 305 310 315 320  
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
 325 330 335  
 25 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly  
 340 345 350  
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
 355 360 365  
 30 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
 370 375 380  
 35 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
 385 390 395 400  
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser  
 405 410 415  
 40 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
 420 425 430  
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys  
 435 440 445  
 45 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
 450 455 460  
 50 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser  
 465 470 475 480  
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu  
 485 490 495  
 55 Ser Gln Asp Ile Lys Leu  
 500

(2) INFORMATION FOR SEQ ID NO:9:

60

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1822 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 49..1341  
 (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"  
 /product= "OP1"  
 /evidence= EXPERIMENTAL  
 /standard\_name= "OP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20	GGTGC	GGGCC	CGGAG	CCCCGG	AGCCC	GGGTA	GCGCG	TAGAG	CCGGC	CGCG	ATG	CAC	GTG	57			
											Met	His	Val				
											1						
25	CGC	TCA	CTG	CGA	GCT	GCG	GCG	CCG	CAC	AGC	TTC	GTG	GCG	CTC	TGG	GCA	105
	Arg	Ser	Leu	Arg	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	Leu	Trp	Ala		
	5					10					15						
30	CCC	CTG	TTC	CTG	CTG	CGC	TCC	GCC	CTG	GCC	GAC	TTC	AGC	CTG	GAC	AAC	153
	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	Leu	Asp	Asn	
	20					25					30					35	
35	GAG	GTG	CAC	TCG	AGC	TTC	ATC	CAC	CGG	CGC	CTC	CGC	AGC	CAG	GAG	CGG	201
	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	Gln	Glu	Arg	
					40				45					50			
40	CGG	GAG	ATG	CAG	CGC	GAG	ATC	CTC	TCC	ATT	TTG	GGC	TTG	CCC	CAC	CGC	249
	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg	
				55				60					65				
45	CTG	GAC	CTG	TAC	AAC	GCC	ATG	GCG	GTG	GAG	GAG	GGC	GGC	GGG	CCC	GGC	345
	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	Gly	Pro	Gly	
	85					90						95					
50	GGC	CAG	GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	393
	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	
	100					105					110					115	
55	CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	441
	Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
					120				125						130		
60	ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	489
	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
				135				140						145			
60	CAC	CCA	CGC	TAC	CAÇ	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	537

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	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
			150					155					160				
5	CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	585
	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
		165					170					175					
10	TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	633
	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
	180					185					190					195	
15	CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
					200					205					210		
20	GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
				215					220					225			
25	ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
			230					235					240				
30	GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
		245					250					255					
35	AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
	260					265					270					275	
40	TTC	ATG	GTG	GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	921
	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	
					280					285					290		
45	CGG	TCC	ACG	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	969
	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	
				295					300					305			
50	AAG	AAC	CAG	GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	1017
	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	
			310					315					320				
55	AGC	GAC	CAG	AGG	CAG	GCC	TGT	AAG	AAG	CAC	GAG	CTG	TAT	GTC	AGC	TTC	1065
	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	
		325					330					335					
60	CGA	GAC	CTG	GGC	TGG	CAG	GAC	TGG	ATC	ATC	GCG	CCT	GAA	GGC	TAC	GCC	1113
	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	
	340					345					350					355	
65	GCC	TAC	TAC	TGT	GAG	GGG	GAG	TGT	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	1161
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	
					360					365					370		
70	AAC	GCC	ACC	AAC	CAC	GCC	ATC	GTG	CAG	ACG	CTG	GTC	CAC	TTC	ATC	AAC	1209
	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	
				375					380					385			
75	CCG	GAA	ACG	GTG	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACG	CAG	CTC	AAT	GCC	1257

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Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala  
 390 395 400

ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA 1305  
 5 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys  
 405 410 415

TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC 1351  
 10 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 420 425 430

GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG 1411

GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG 1471  
 15 TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC 1531

ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC 1591

GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651  
 20 CGTTTCCAGA GGTAATTATG AGCGCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711

GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATGAC CCGGAAGTTC 1771  
 25 CTGTAATAAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala  
 1 5 10 15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser  
 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser  
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu  
 50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro  
 65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly  
 85 90 95

Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser  
 100 105 110

60



(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= OPX  
/note= "Each Xaa is independently selected from  
a group of one or more specified amino acids  
as defined in the specification"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1          5          10          15
Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20          25          30
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35          40          45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
50          55          60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65          70          75          80
Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85          90          95
Xaa Ala Cys Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

28

GCGGATCCTG TTGTGAAGGN AATATGTG

(2) INFORMATION FOR SEQ ID NO:13:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

24

20 GCGATCCGTC GCAGTCAAAA TTTT

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

26

40 GCGGATCCGC GATATATTAA AAGCAA

(2) INFORMATION FOR SEQ ID NO:15:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20

60 .CGGAATTCTG GTGCCATATA

030304-0100  
T00T0T "E42E650